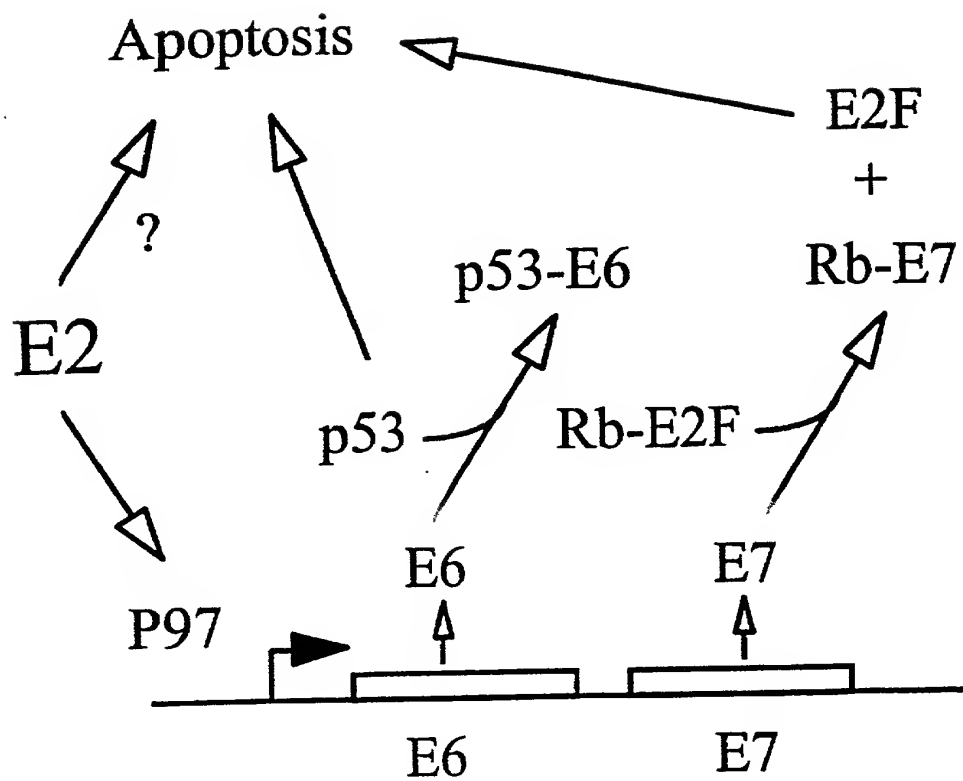


Fig. 1

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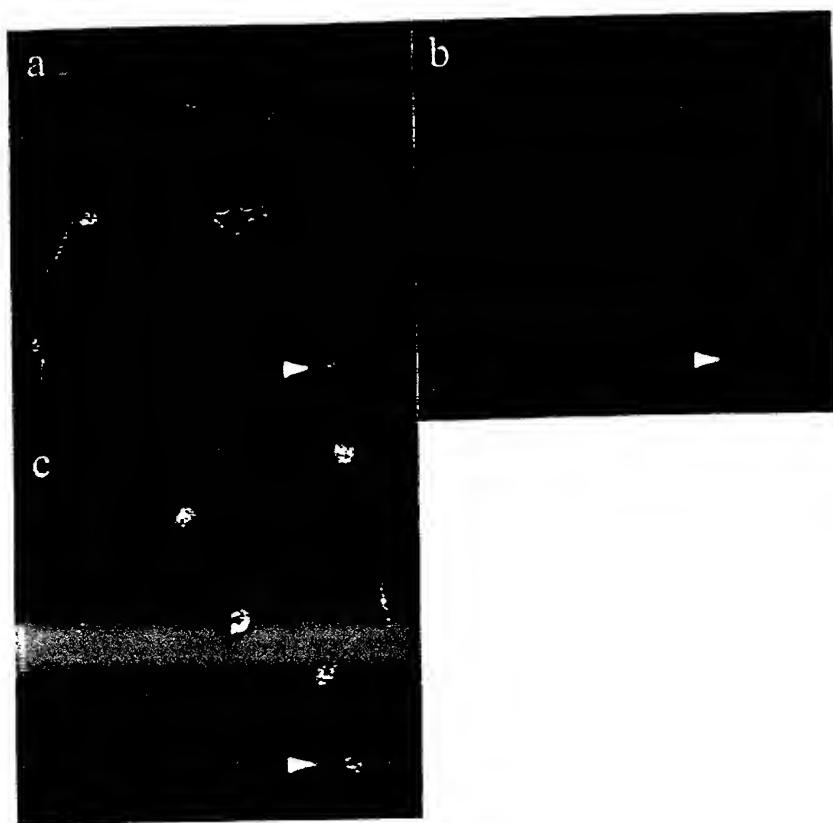
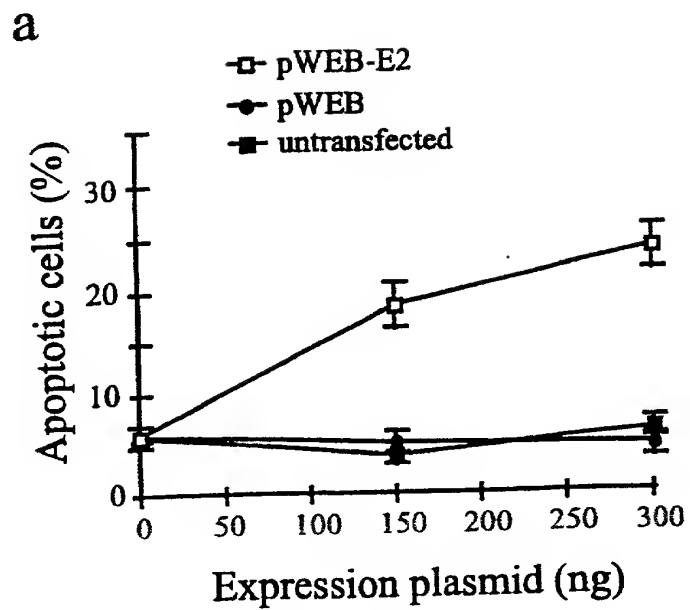


Fig. 2

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Fig. 3A



b

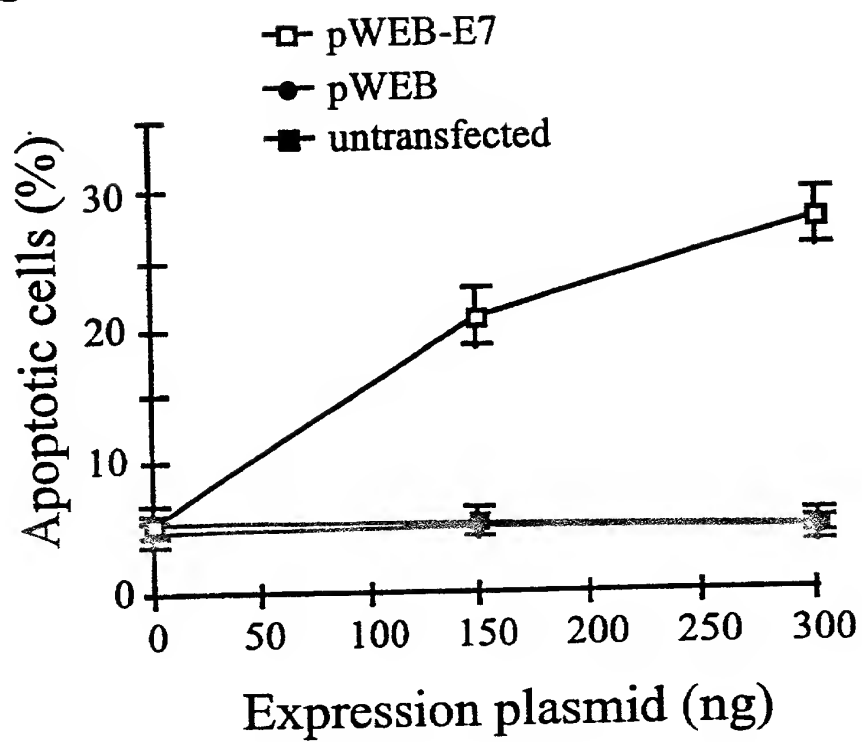


Fig. 3B

Fig. 4

a

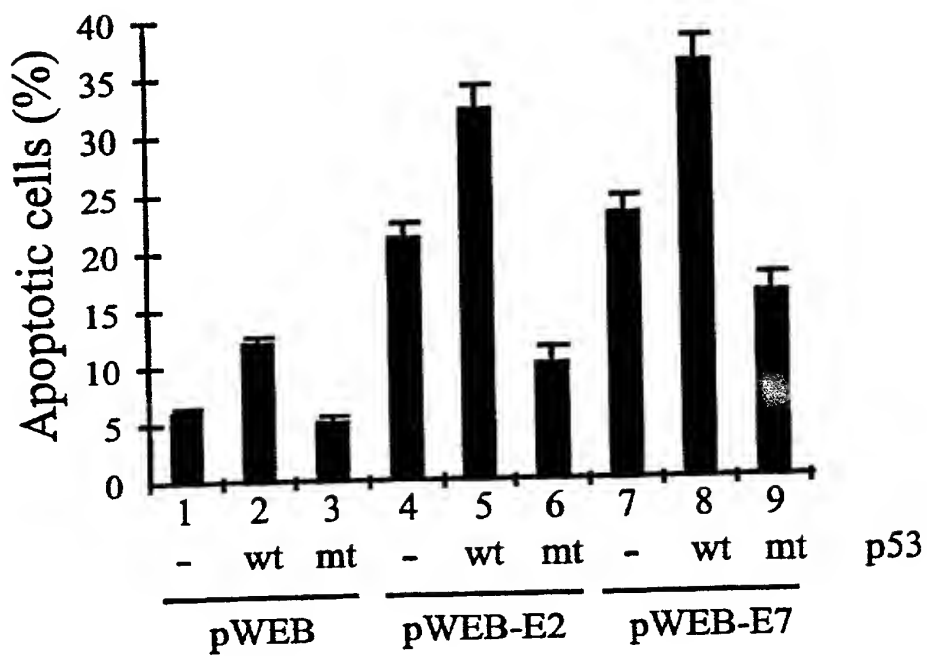


Fig. 4B

b

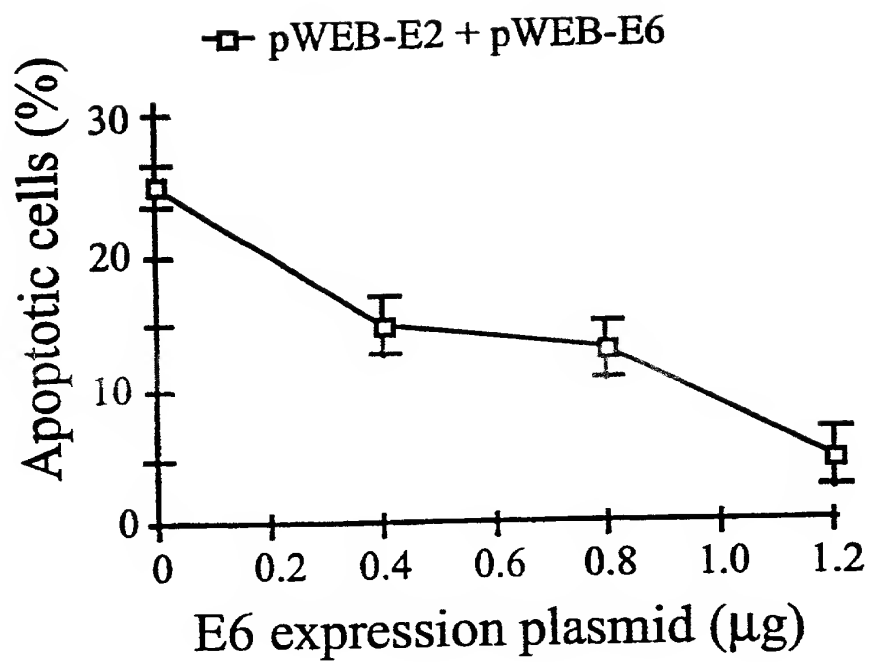
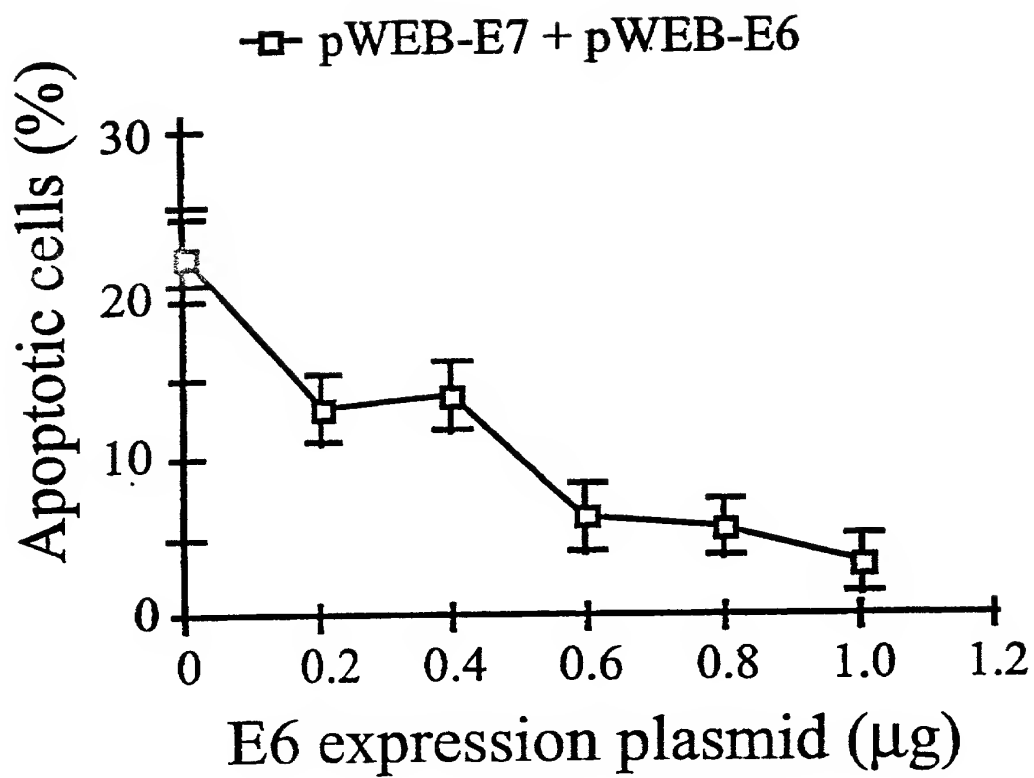


Fig 4C

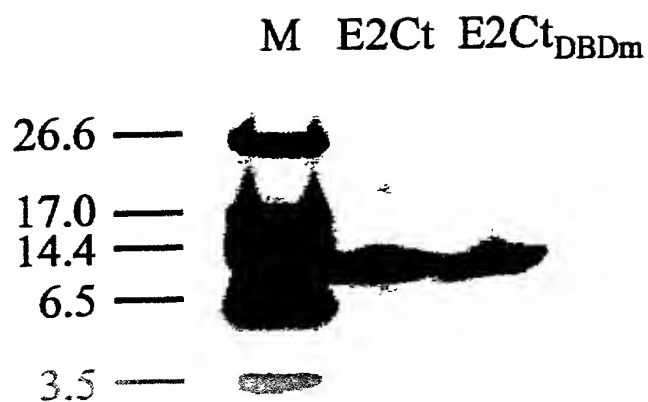
C



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Fig 5A

a



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Fig 5B

b

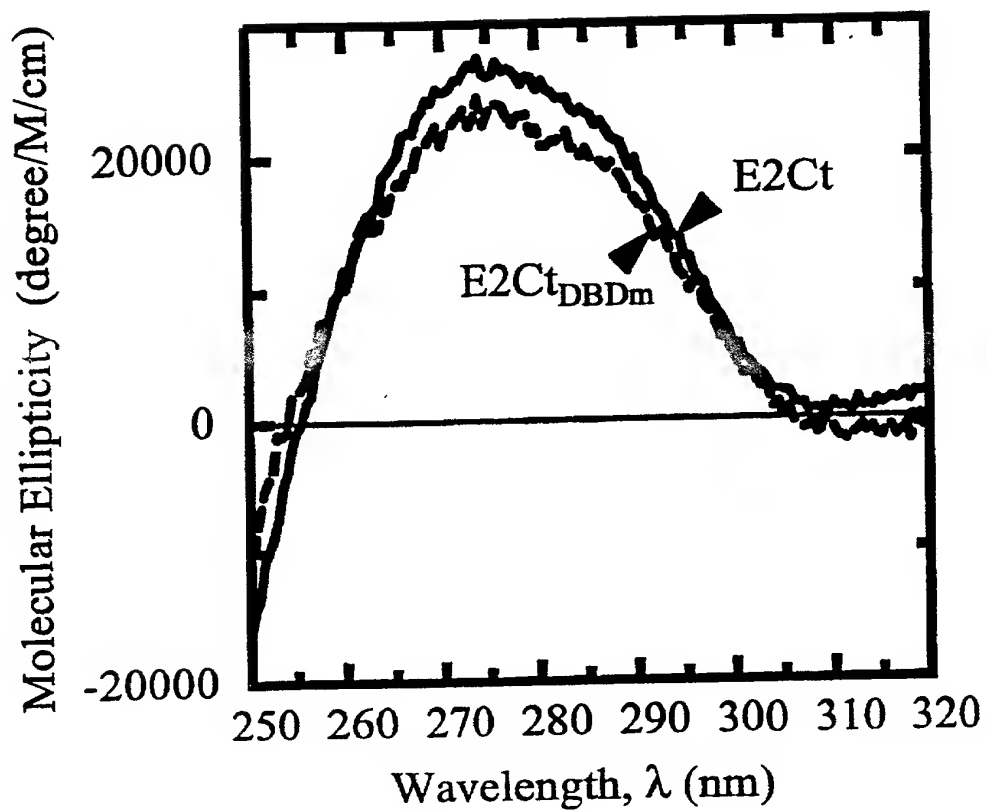


Fig 5C

C

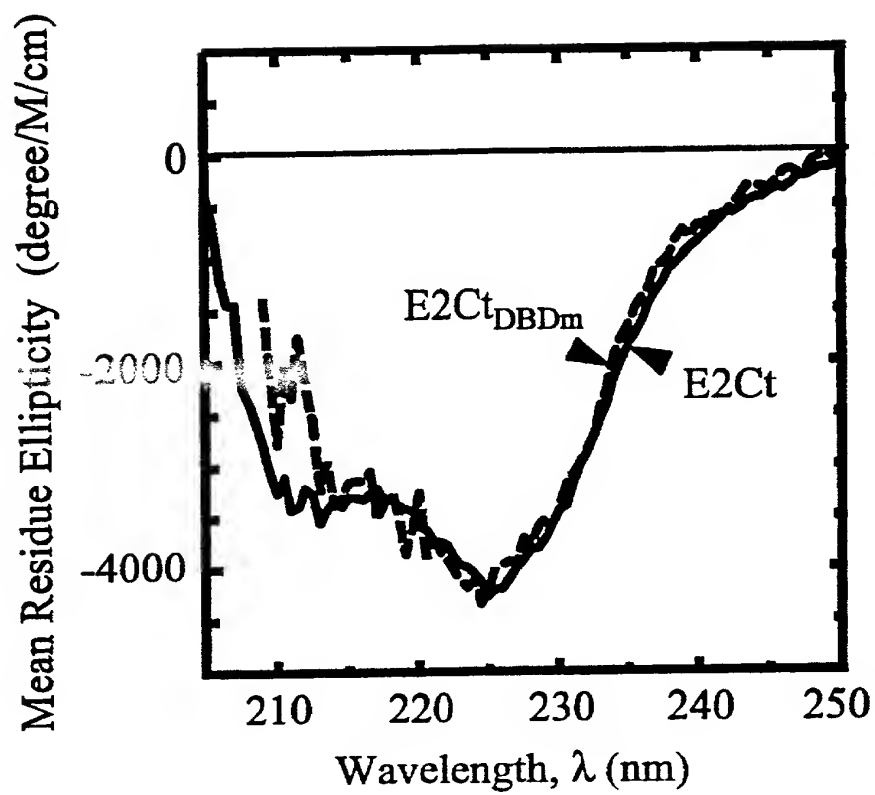
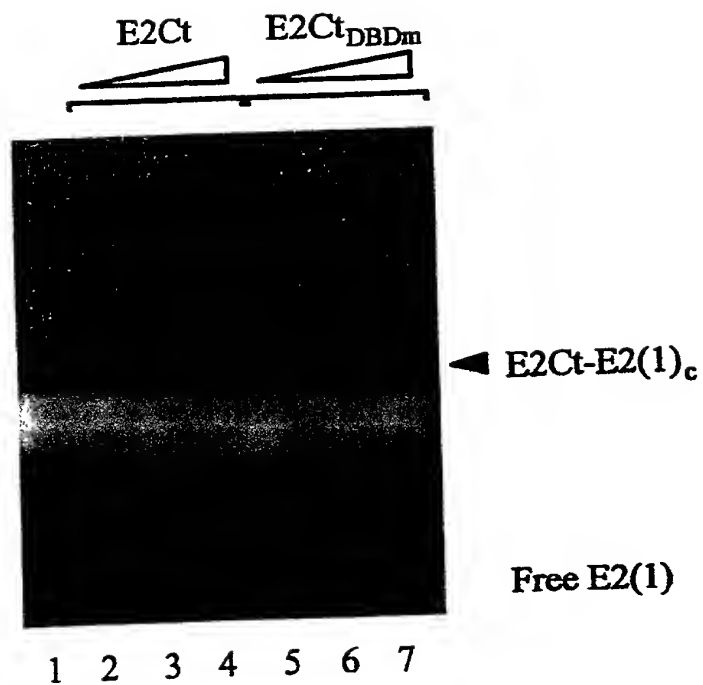


Fig 5D

d



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Fig. 6

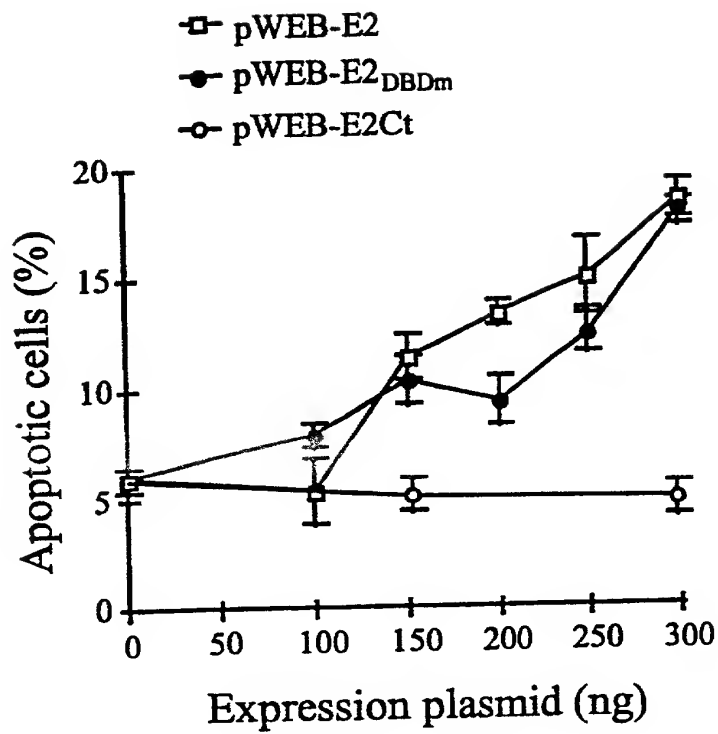
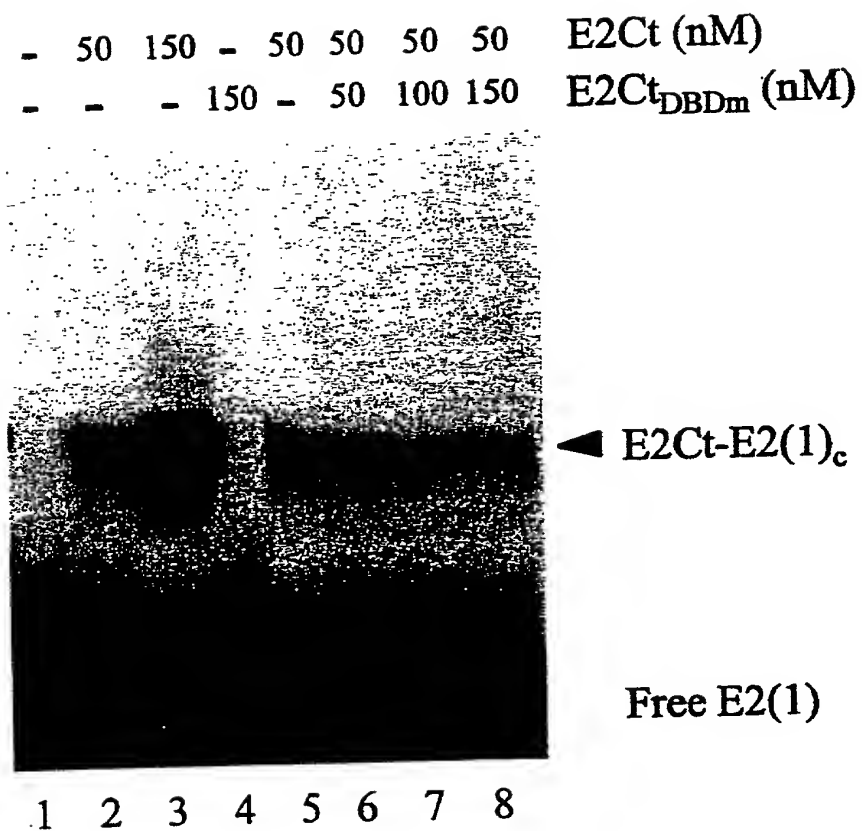


Fig. 7A

a



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Fig. 7B

b

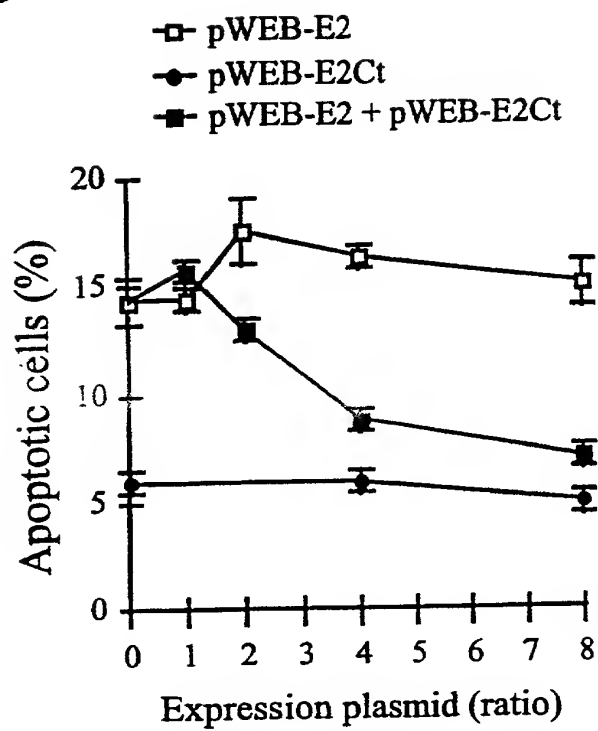


Fig. 8

The E2 proteins used in this work

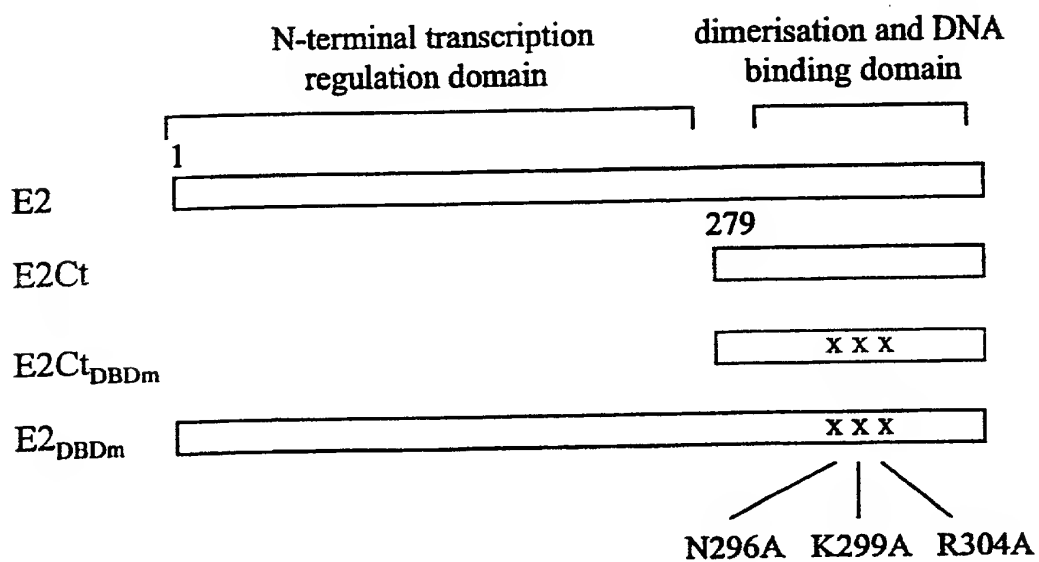


Fig. 9

HPV 16 E2

2755 ATGGGAGACTCTTTGCCAACGTTTAAATGTGTGTGTCAGGACAAAATACTAACACATTATGAA
-----+-----+-----+-----+-----+-----+-----+-----
M E T L C Q R L N V C Q D K I L T H Y E

2815 AATGATAGTACAGACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
-----+-----+-----+-----+-----+-----+-----+-----
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTTAAACATATTAACCACCAAGTGGTGCCA

2875 -----+-----+-----+-----+-----+-----+-----+-----
A I Y Y K A R E M G F K H I N H Q V V P

2935 ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
-----+-----+-----+-----+-----+-----+-----+-----
T L A V S K N K A L Q A I E L Q L T L E

2995 ACAATATATAACTCACAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
-----+-----+-----+-----+-----+-----+-----+-----
T I Y N S Q Y S N E K W T L Q D V S L E

3055 GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGGAAGTGCAG
-----+-----+-----+-----+-----+-----+-----+-----
V Y L T A P T G C I K K H G Y T V E V Q

3115 TTTGATGGAGACATATGCAATACAATGCATTATACAAACTGGACACATATATATATTTGT
-----+-----+-----+-----+-----+-----+-----+-----
F D G D I C N T M H Y T N W T H I Y I C

3175 GAAGAAGCATCAGTAAGTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTATATTATGTT
-----+-----+-----+-----+-----+-----+-----+-----
E E A S V T V V E G Q V D Y Y G L Y Y V

3235 CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAAA
-----+-----+-----+-----+-----+-----+-----+-----
H E G I R T Y F V Q F K D D A E K Y S K

3295 AATAAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
-----+-----+-----+-----+-----+-----+-----+-----
N K V W E V H A G G Q V I L C P T S V F

3355 AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
-----+-----+-----+-----+-----+-----+-----+-----
S S N E V S S P E I I R Q H L A N H P A

3415 GCGACCCATACCAAAGCCGTCGCCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
-----+-----+-----+-----+-----+-----+-----+-----

10047990-011402

A T H T K A V A L G T E E T Q T T I Q R

3475 CCAAGATCAGAGCCAGACACCGGAAACCCCTGCCACACCACTAAGTTGTTGCACAGAGAC
-----+-----+-----+-----+-----+-----+-----
P R S E P D T G N P C H T T K L L H R D

3535 TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAC
-----+-----+-----+-----+-----+-----+-----
S V D S A P I L T A F N S S H K G R I N

3595 TGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAATGT
-----+-----+-----+-----+-----+-----+-----
C N S N T T P I V H L K G D A N T L K C

3655 TTAAGATATAGATTTAAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

3715 TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

3775 TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACCTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

3835 GGATTTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

E04F10"066400T

Fig 10

HPV 16 E2DBDm

ATGGAGACTCTTTGCCAACGTTTAAATGTGTGTCAGGACAAAATACTAACACATTATGAA
2755 -----+-----+-----+-----+-----+-----+-----+-----
M E T L C Q R L N V C Q D K I L T H Y E

AATGATAGTACAGACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
2815 -----+-----+-----+-----+-----+-----+-----+-----
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTAAACATATTAACCACCAAGTGGTGCCA
2875 -----+-----+-----+-----+-----+-----+-----+-----
A I Y Y K A R E M G F K H I N H Q V V P

ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
2935 -----+-----+-----+-----+-----+-----+-----+-----
T L A V S K N K A L Q A I E L Q L T L E

ACAATATATAACTCACAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
2995 -----+-----+-----+-----+-----+-----+-----+-----
T I Y N S Q Y S N E K W T L Q D V S L E

GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGAAGTGCAG
3055 -----+-----+-----+-----+-----+-----+-----+-----
V Y L T A P T G C I K K H G Y T V E V Q

TTTGTATGGAGACATATGCAATACAATGCATTATACAACTGGACACATATATATTTGT
3115 -----+-----+-----+-----+-----+-----+-----+-----
F D G D I C N T M H Y T N W T H I Y I C

GAAGAAGCATCAGTAACTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTATATTATGTT
3175 -----+-----+-----+-----+-----+-----+-----+-----
E E A S V T V V E G Q V D Y Y G L Y Y V

CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAAA
3235 -----+-----+-----+-----+-----+-----+-----+-----
H E G I R T Y F V Q F K D D A E K Y S K

AATAAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
3295 -----+-----+-----+-----+-----+-----+-----+-----
N K V W E V H A G G Q V I L C P T S V F

AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
3355 -----+-----+-----+-----+-----+-----+-----+-----
S S N E V S S P E I I R Q H L A N H P A

GCGACCCATACCAAAGCCGTCGCCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
3415 -----+-----+-----+-----+-----+-----+-----+-----
A T H T K A V A L G T E E T Q T T I Q R

204470-06924001

3475 CCAAGATCAGAGCCAGACACCGGAAACCCCTGCCACACCACTAAGTTGTTGCACAGAGAC
-----+-----+-----+-----+-----+-----+-----
P R S E P D T G N P C H T T K L L H R D

3535 TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAAC
-----+-----+-----+-----+-----+-----+-----
S V D S A P I L T A F N S S H K G R I N

3595 TGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTgctACTTTAgcaTGT
-----+-----+-----+-----+-----+-----+-----
C N S N T T P I V H L K G D A A T L A C

3655 TTAAGATATgcaTTTAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----
L R Y A F K K H C T L Y T A V S S T W H

3715 TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

3775 TGGCAACGTGACCAATTTTGTCTCAAGTTAAAATACCAAAAACATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

3835 GGATTTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

204740 06624007

Fig 11

E2Ct

ATGAACTGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAAATGT
-----+-----+-----+-----+-----+-----+-----
M N C N S N T T P I V H L K G D A N T L K C

TTAAGATATAGATTTAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAATATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

GGATTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

204470 066400T

Fig 12

E2CtDBDm

```
ATGAACTGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTgctACTTTAgcaTGT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
M N C N S N T T P I V H L K G D A A T L A C

TTAAGATATgcaTTTAAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
L R Y A F K K H C T L Y T A V S S T W H

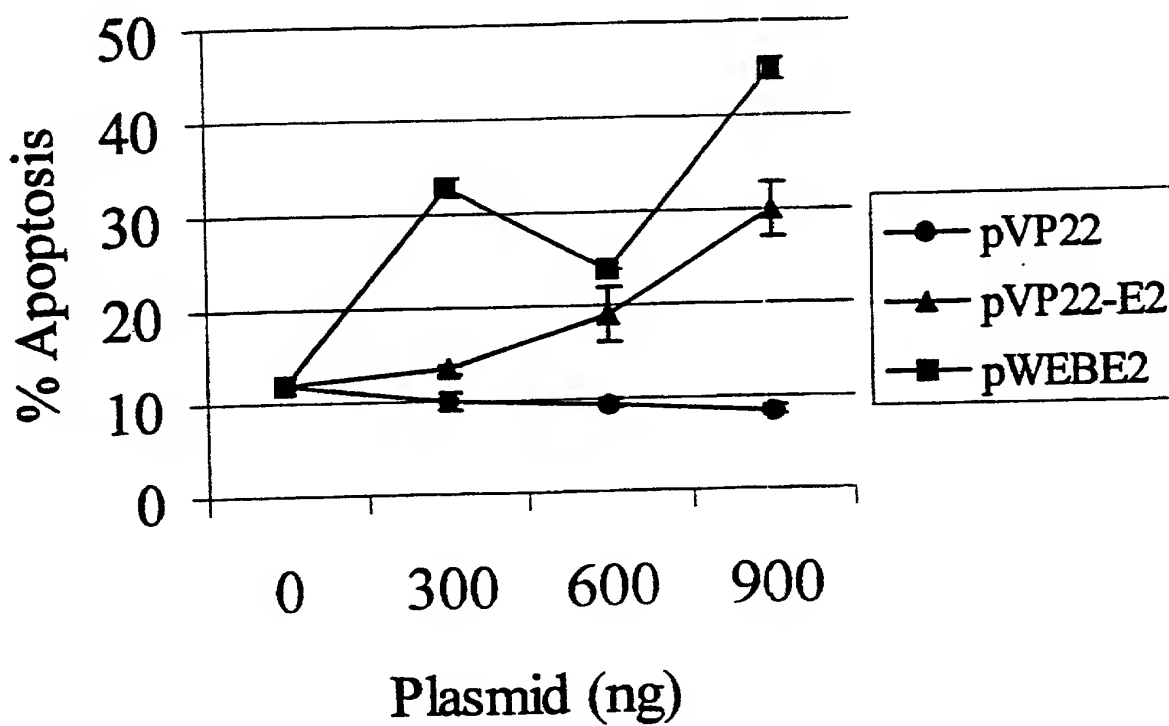
TGGACAGGACATAATGTAAACATAAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+
W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTGTCTCAAGTTAAATACCAAAAACTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
W Q R D Q F L S Q V K I P K T I T V S T

GGATTTATGTCTATATGA
-----+-----+-----+-----+-----+-----+-----+-----+-----+
G F M S I * - 3852
```

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Fig 13



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